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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/551,977	10/04/2005	David Deperthes	KZI-002US	3931
959 7590 02/08/2007 LAHIVE & COCKFIELD, LLP ONE POST OFFICE SQUARE BOSTON, MA 02109-2127			EXAMINER GUSSOW, ANNE	
			ART UNIT	PAPER NUMBER
			1643	
SHORTENED STATUTORY PERIOD OF RESPONSE		MAIL DATE	DELIVERY MODE	
30 DAYS		02/08/2007	PAPER	

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.



UNITED STATES DEPARTMENT OF COMMERCE

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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
10/551,997	10/24/05	Depertthes, et al	KZI-00245

EXAMINER

Anne M. Gussow

ART UNIT

PAPER

1643

20070201

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

1. The reply filed 1/11/07, is not fully responsive to the communication mailed 12/12/06 for the reasons set forth on the attached Raw Sequence Listing Error Report.
2. Since the above-mentioned reply appears to be bona fide, applicant is given a TIME PERIOD of ONE (1) MONTH or THIRTY (30) DAYS, from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME LIMIT MAY BE GRANTED UNDER 37 CFR 1.136(a).
3. Any inquiry concerning this communication should be directed to Examiner Anne M. Gussow, Ph.D. Art Unit 1643, whose telephone number is (571)272-6047. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196. Any questions regarding compliance with the sequence rules requirements specifically should be directed to the departments listed at the bottom of the Notice to Comply.

Notice to Comply and
Sequence Error Report
Attached


LARRY R. HELMS, PH.D.
SUPERVISORY PATENT EXAMINER

Notice to Comply	Application No. 10/551,977	Applicant(s) Deperthes, et al.	
	Examiner Anne M. Gussow	Art Unit 1643	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e). The correct SEQ ID NO:2 is present in the paper copy of the of the sequence listing only. Therefore a search of the correct sequence is not possible.
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", **as well as an amendment specifically directing its entry into the application.**
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216 or (703) 308-2923

For CRF Submission Help, call (703) 308-4212 or 308-2923

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/551,977A
Source: FW16
Date Processed by STIC: 7/18/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/551,977A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 01/18/2007

PATENT APPLICATION: US/10/551,977A

TIME: 10:42:16

Input Set : A:\SeqList.txt

Output Set: N:\CRF4\01182007\J551977A.raw

4 <110> APPLICANT: DEPERTHES, David
 5 CLOUTIER, Sylvain
 6 MACH, Jean-Pierre
 7 HOLLER, Nils
 8 FATTAH, Omar
 10 <120> TITLE OF INVENTION: PEPTABODY FOR CANCER TREATMENT
 12 <130> FILE REFERENCE: KZI-002US
 14 <140> CURRENT APPLICATION NUMBER: 10/551977A
 15 <141> CURRENT FILING DATE: 2005-10-04
 17 <150> PRIOR APPLICATION NUMBER: PCT/IB2004/001049
 18 <151> PRIOR FILING DATE: 2004-04-05
 20 <150> PRIOR APPLICATION NUMBER: US 60/460,490
 21 <151> PRIOR FILING DATE: 2003-04-04
 23 <160> NUMBER OF SEQ ID NOS: 30
 25 <170> SOFTWARE: PatentIn version 3.1

see pp. 1-2
 Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

131 <210> SEQ ID NO: 6
 132 <211> LENGTH: 6
 133 <212> TYPE: DNA *delete - this is not a DNA sequence*
 134 <212> TYPE: PRT
 135 <213> ORGANISM: Artificial sequence
 137 <220> FEATURE:
 138 <223> OTHER INFORMATION: Enhancer Peptide
 140 <400> SEQUENCE: 6
 141 Tyr Ser Phe Glu Asp Leu
 E--> 142 1 *5* *misaligned amino acid numbers (see item 3 on Error summary sheet)*
 144 <210> SEQ ID NO: 7
 145 <211> LENGTH: 7
 146 <212> TYPE: PRT
 147 <213> ORGANISM: Artificial sequence
 149 <220> FEATURE:
 150 <223> OTHER INFORMATION: Enhancer Peptide
 152 <400> SEQUENCE: 7
 153 Tyr Ser Phe Glu Asp Leu Tyr
 E--> 154 1 *5* *same error*
 156 <210> SEQ ID NO: 8
 157 <211> LENGTH: 8
 158 <212> TYPE: PRT
 159 <213> ORGANISM: Artificial sequence
 161 <220> FEATURE:

RAW SEQUENCE LISTING

DATE: 01/18/2007

PATENT APPLICATION: US/10/551,977A

TIME: 10:42:16

Input Set : A:\SeqList.txt

Output Set: N:\CRF4\01182007\J551977A.raw

```

162 <223> OTHER INFORMATION: Enhancer Peptide
164 <400> SEQUENCE: 8
165 Tyr Ser Phe Glu Asp Leu Tyr Arg
E--> 166 1      5      SE same exon
168 <210> SEQ ID NO: 9
169 <211> LENGTH: 9
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Enhancer Peptide
176 <400> SEQUENCE: 9
177 Tyr Ser Phe Glu Asp Leu Tyr Arg Arg
E--> 178 1      5      5 ←
191 <210> SEQ ID NO: 11
192 <211> LENGTH: 25
193 <212> TYPE: PRT
194 <213> ORGANISM: Spodoptera litura
196 <400> SEQUENCE: 11
197 Glu Asn Phe Ser Gly Gly Cys Val Ala Gly Tyr Met Arg Thr Pro Asp
198 1      5      10      15
199 Gly Arg Cys Lys Pro Thr Phe Tyr Gln
E--> 200 20-25      20      25 ←

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/551,977A

DATE: 01/18/2007

TIME: 10:42:17

Input Set : A:\SeqList.txt

Output Set: N:\CRF4\01182007\J551977A.raw

L:102 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:100
L:134 M:280 W: Numeric Identifier already exists, Type not replaced.
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:142 M:301 E: (44) No Sequence Data was Shown, SEQ ID:6
L:142 M:252 E: No. of Seq. differs, <211> LENGTH:Input:6 Found:0 SEQ:6
L:154 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:166 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:178 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:200 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11